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OM nucleic - nucleic search, using sw model!

Run on: July 9, 2005, 10:46:10 ; Search time 192.141 Seconds
(without alignments)

9120.6666 Million cell updates/sec

Title: US-09-938-842A-1034

Perfect score: 1071

Sequence: 1 atggcacaattccaaaggct.....cacggtcatcgaaacctga 1071

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq;*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq;*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq;*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq;*

5: /cgn2_6/ptodata/1/ina/PCITS_COMB.seq;*

6: /cgn2_6/ptodata/1/ina/backfile.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	4.1	44	4.1	7218	1	US-09-2322463-14	Sequence 14, Appli
c 2	4.1	41	3.8	7218	1	US-08-2322463-14	Sequence 14, Appli
c 3	40.4	3.8	915	4	US-09-2488796A-6057	Sequence 6057, Appli	
c 4	3.4	3.2	654	4	US-08-956171B-613	Sequence 613, Appli	
c 5	34	3.2	654	4	US-08-761-988A-613	Sequence 613, Appli	
c 6	33.4	3.1	601	4	US-09-949-016-133921	Sequence 33921, Appli	
c 7	33.4	3.1	601	4	US-09-949-016-133049	Sequence 133049, Appli	
c 8	33.4	3.1	34068	4	US-09-949-016-154849	Sequence 154849, Appli	
c 9	33.4	3.1	51711	4	US-09-949-016-125599	Sequence 125599, Appli	
c 10	33	3.1	2127	4	US-09-252-991A-8192	Sequence 8192, Appli	
c 11	33	3.1	2874	4	US-09-252-991A-8112	Sequence 8112, Appli	
c 12	32.8	3.1	4403765	3	US-09-103-80A-2	Sequence 2, Appli	
c 13	32.2	3.0	2406	4	US-09-632-098-5	Sequence 5, Appli	
c 14	32.2	3.0	2406	4	US-10-177-308-5	Sequence 5, Appli	
c 15	32.2	3.0	2439	3	US-09-632-098-6	Sequence 6, Appli	
c 16	32.2	3.0	2439	4	US-10-177-308-6	Sequence 6, Appli	
c 17	31.6	3.0	601	4	US-09-949-016-121693	Sequence 121693, Appli	
c 18	31.6	3.0	601	4	US-09-949-016-121694	Sequence 121694, Appli	
c 19	31.6	3.0	601	4	US-09-949-016-121695	Sequence 121695, Appli	
c 20	31.6	3.0	1104	4	US-09-802-540-6871	Sequence 6871, Appli	
c 21	31.6	3.0	1141	4	US-09-808B-22	Sequence 22, Appli	
c 22	31.6	3.0	4019	4	US-09-902-540-583	Sequence 583, Appli	
c 23	31.6	3.0	15192	4	US-09-949-016-15143	Sequence 15143, Appli	
c 24	31.4	2.9	4411529	3	US-09-103-80A-1	Sequence 1, Appli	
c 25	2.9	3842	4	US-09-976-594-279	Sequence 279, Appli		
c 26	30.6	2.9	412	3	US-08-981-083-111	Sequence 111, Appli	
c 27	30.6	2.9	412	4	US-09-5336-784-111	Sequence 111, Appli	

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367

GENERAL INFORMATION:
/ APPLICANT: DORNER, P.
/ APPLICANT: SCHEIFLINGER, F.
/ APPLICANT: FALKNER, F. G.
/ TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEES: Foley & Lardner
/ STREET: 1800 Diagonal Road, Suite 500
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22313-0299

COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ COMPUTER READABLE FORM:
/ APPLICATION NUMBER: US/08/232,463
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/935,313
/ FILING DATE:
/ APPLICATION NUMBER: EP 91 114 300.6
/ FILING DATE: 26-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ TELEPHONE: (703) 683-4109
/ TELEFAX: (703) 683-4109
/ TELEX: 99119
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7118 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: PTZ9PT-F18
/ US-08-232-463-14
Query Match 4.1%; Score 44; DB 1; Length 7218;

Db 655 ATTATGATGCTGCTATCTGTGGTAACCTCCCTGCTATGGTCTCCAGAACCTTG 714
 Qy 907 TCGTTTATGGCTCC 920
 Db 715 GCTGCTTGGCTGC 728

RESULT 4
 US-08-956-171E-613/C
 Sequence 613, Application US/08956171E
 Patent No. 6593114
 GENERAL INFORMATION:
 APPLICANT: Charles Kunisch
 Gail H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Bannon
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956,171E
 FILING DATE: 20-OCT-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/781,986
 FILING DATE: January 3, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224
 TELEFAX: (301) 309-8439
 INFORMATION FOR SEQ ID NO: 613:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 654 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 613:

US-08-956-171E-613
 Query Match 3.2%; Score 34; DB 4; Length 654;
 Best Local Similarity 48.0%; Pred. No. 1.3;
 Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
 Qy 472 ATGGGTAAAATCTGATGAAAGAAAACGTTAACGACCTCTAACGTGACTATAGAC 531
 Db 455 ATACTGCAATTGATAGATAAAAGATAAAAGATAATAGCCAAAATCTGGCTTAATGCC 396
 Qy 532 ATAGGCACCGAAATTCGGGACTAATAGCTTAACTGCTTAACTGCTCAATTGCAAGACATC 591
 Db 395 TTAGGGCATAGCTTCTTCTGGCTCATCTGATTCACCTGAGCTTACTCTGTGA 336
 Qy 592 CAACCTCGGAAAGCTCTGGCATCATCACAATGCTGCGCAAGGAATG 651
 Db 335 CCACCAACCGAAATTCGGGACTAATATACTGCTTAAGANACAGATAACCCNACA 276
 Qy 652 TATCCGATGCTGGCTTACATCACAATGCTGCGCAAGGAATG 673
 Db 275 AACGGTGTCTGGCTTGTAT 254

RESULT 5
 US-08-781-986A-613/C
 Sequence 613, Application US/08781986A
 Patent No. 6737248
 GENERAL INFORMATION:
 APPLICANT: Charles Kunisch
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5255
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PB248P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 613:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 654 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-613

Query Match 3.2%; Score 34; DB 4; Length 654;
 Best Local Similarity 48.0%; Pred. No. 1.3;
 Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
 Qy 472 ATGGGTAAAATCTGATGAAAGAAAACGTTAACGACCTCTAACGTGACTATAGAC 531
 Db 455 ATACTGCAATTGATAGATAAAAGATAAAAGATAATAGCCAAAATCTGGCTTAATGCC 396
 Qy 532 ATAGGCACCGAAATTCGGGACTAATAGCTTAACTGCTCAATTGCAAGACATC 591
 Db 395 TTAGGGCATAGCTTCTTCTGGCTCATCTGATTCACCTGAGCTTACTCTGTGA 336
 Qy 592 CAACCTCGGAAAGCTCTGGCATCATCACAATGCTGCGCAAGGAATG 651
 Db 335 CCACCAACCGAAATTCGGGACTAATATACTGCTTAAGANACAGATAACCCNACA 276
 Qy 652 TATCCGATGCTGGCTTACATCACAATGCTGCGCAAGGAATG 673
 Db 275 AACGGTGTCTGGCTTGTAT 254

RESULT 6
 US-09-949-016-33921
 Sequence 33921, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CJO01307

CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231, 498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 33921
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-33921

Query Match 3.1%; Score 33.4%; DB 4; Length 601;
 Best Local Similarity 53.4%; Pred. No. 1.9;
 Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 29 TTGCAGGCAAAAGATCAAACTCTAAGACGGTGTGATCAACCATCATCAACGGCGTCAAGAA 88
 Db 100 TTGCAGGCAAAAGATCAAACTCTAAGACGGTGTGATCAACCATCATCAACGGCGTCAAGAA 159

Qy 89 AGCTCGAACTCAAGACTTCCAACTAAATCCCACAGTGAAGTCAGTCAGTCAAGTCTCGAGCTGATCAAGGCGG 148
 Db 160 TGTCACTCTGAAAGAGAGCACTACACATCGGGCTGAGCAGCACTGGGCTGAGCAGAGGG 219

Qy 149 AGCCGTGATG 159
 Db 220 ACCAGGCGATG 230

RESULT 7
 US-09-949-016-133049
 / Sequence 133049, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CJO01307

CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 133049
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-133049

Query Match 3.1%; Score 33.4%; DB 4; Length 601;
 Best Local Similarity 53.4%; Pred. No. 1.9;
 Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 29 TTGCAGGCAAAAGATCAAACTCTAAGACGGTGTGATCAACCATCATCAACGGCGTCAAGAA 88
 Db 100 TTGCAGGCAAAAGATCAAACTCTAAGACGGTGTGATCAACCATCATCAACGGCGTCAAGAA 159

Qy 89 AGCTCGAACTCAAGACTTCCAACTAAATCCCACAGTGAAGTCAGTCAGTCAAGTCTCGAGCTGATCAAGGCGG 148
 Db 160 TGTCACTCTGAAAGAGAGCACTACACATCGGGCTGAGCAGCACTGGGCTGAGCAGAGGG 219

Qy 149 AGCCGTGATG 159
 Db 220 ACCAGGCGATG 230

RESULT 8
 US-09-949-016-15489/c
 / Sequence 15489, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CJO01307

CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 15489

Query Match 3.1%; Score 33.4%; DB 4; Length 34068;
 Best Local Similarity 53.4%; Pred. No. 21;
 Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 29 TTGCAGGCAAAAGATCAAACTCTAAGACGGCGTGTGATCAACCATCATCAACGGCGTCAAGAA 88
 Db 16953 TTGCAGGCAAAAGATCAAACTCTAAGACGGCGTGTGATCAACCATCATCAACGGCGTCAAGAA 16894

Qy 89 AGCTCGAACTCAAGACTTCCAACTAAATCCCACAGTGAAGTCAGTCAGTCAAGTCTCGAGCTGATCAAGGCGG 148
 Db 16893 TGTCACTCTGAAAGAGAGCACTACACATCGGGCTGAGCAGCACTGGGCTGAGCAGAGGG 16893

Qy 149 AGCCGTGATG 159
 Db 16833 AGCCGTGATG 16823

RESULT 9
 US-09-949-016-12559/c
 / Sequence 12559, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CJO01307

CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 13049

Query Match 3.1%; Score 33.4%; DB 4; Length 601;
 Best Local Similarity 53.4%; Pred. No. 1.9;
 Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 29 TTGCAGGCAAAAGATCAAACTCTAAGACGGCGTGTGATCAACCATCATCAACGGCGTCAAGAA 88
 Db 100 TTGCAGGCAAAAGATCAAACTCTAAGACGGCGTGTGATCAACCATCATCAACGGCGTCAAGAA 159

Qy 89 AGCTCGAACTCAAGACTTCCAACTAAATCCCACAGTGAAGTCAGTCAGTCAAGTCTCGAGCTGATCAAGGCGG 148
 Db 160 TGTCACTCTGAAAGAGAGCACTACACATCGGGCTGAGCAGCACTGGGCTGAGCAGAGGG 219

Qy 89 AGCTCGAACTCAAGACTTCCAACTAAATCCCACAGTGAAGTCAGTCAGTCAAGTCTCGAGCTGATCAAGGCGG 148
 Db 160 TGTCACTCTGAAAGAGAGCACTACACATCGGGCTGAGCAGCACTGGGCTGAGCAGAGGG 219

Query Match Score 33.4%; DB 4; Length 51711;
 Best Local Similarity 53.4%; Pred. No. 27;
 Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
 SEQ ID NO: 8112 LENGTH: 2874 TYPE: DNA
 ORGANISM: *Pseudomonas aeruginosa*
 FEATURE: NAME/KEY: unsure
 LOCATION: (2266)
 OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
 US-09-252-991A-8112

Query Match Score 3.1%; DB 4; Length 2874;
 Best Local Similarity 49.2%; Pred. No. 6.5;
 Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
 SEQ ID NO: 33142 LENGTH: 2874 TYPE: DNA
 ORGANISM: *Pseudomonas aeruginosa*
 FEATURE: NAME/KEY: unsure
 LOCATION: (2266)
 OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
 US-09-252-991A-8112

Query Match Score 3.1%; DB 4; Length 2874;
 Best Local Similarity 49.2%; Pred. No. 6.5;
 Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
 SEQ ID NO: 34466 LENGTH: 2874 TYPE: DNA
 ORGANISM: *Pseudomonas aeruginosa*
 FEATURE: NAME/KEY: unsure
 LOCATION: (2266)
 OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
 US-09-252-991A-8112

Query Match Score 3.1%; DB 4; Length 2874;
 Best Local Similarity 49.2%; Pred. No. 6.5;
 Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
 SEQ ID NO: 34476 LENGTH: 2874 TYPE: DNA
 ORGANISM: *Pseudomonas aeruginosa*
 FEATURE: NAME/KEY: unsure
 LOCATION: (2266)
 OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
 US-09-252-991A-8112

RESULT 10
 US-09-252-991A-8192
 Sequence 8192, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: MARC J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
 TITLE OF INVENTION: *AERUGINOSA* FOR DIAGNOSTICS AND THERAPEUTICS
 FILE NUMBER: 107196-136
 FILE REFERENCE: 287
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/074, 788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094, 190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 8192 LENGTH: 2127
 TYPE: DNA
 ORGANISM: *Pseudomonas aeruginosa*
 FEATURE: NAME/KEY: unsure
 LOCATION: (291)
 OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
 US-09-252-991A-8192

Query Match Score 3.1%; DB 4; Length 2127;
 Best Local Similarity 49.2%; Pred. No. 5.5;
 Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
 SEQ ID NO: 2 LENGTH: 2127 TYPE: DNA
 ORGANISM: *Mycobacterium tuberculosis*
 FEATURE: NAME/KEY: unsure
 LOCATION: (291)
 OTHER INFORMATION: DNA SEQUENCES FOR STRAIN ANALYSIS IN *MYCOBACTERIUM*
 FILE REFERENCE: 24346-20007.00
 CURRENT APPLICATION NUMBER: US/09/103, 840A
 CURRENT FILING DATE: 1998-06-24
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2 LENGTH: 4403765
 TYPE: DNA
 ORGANISM: *Mycobacterium tuberculosis*
 FEATURE: NAME/KEY: unsure
 LOCATION: (291)
 OTHER INFORMATION: CDC 1551
 OTHER INFORMATION: "n" bases at various positions throughout the sequence
 OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Query Match Score 3.1%; DB 4; Length 2127;
 Best Local Similarity 49.2%; Pred. No. 5.5;
 Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
 SEQ ID NO: 2 LENGTH: 2127 TYPE: DNA
 ORGANISM: *Mycobacterium tuberculosis*
 FEATURE: NAME/KEY: unsure
 LOCATION: (291)
 OTHER INFORMATION: DNA SEQUENCES FOR STRAIN ANALYSIS IN *MYCOBACTERIUM*
 FILE REFERENCE: 24346-20007.00
 CURRENT APPLICATION NUMBER: US/09/103, 840A
 CURRENT FILING DATE: 1998-06-24
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2 LENGTH: 4403765
 TYPE: DNA
 ORGANISM: *Mycobacterium tuberculosis*
 FEATURE: NAME/KEY: unsure
 LOCATION: (291)
 OTHER INFORMATION: CDC 1551
 OTHER INFORMATION: "n" bases at various positions throughout the sequence
 OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

RESULT 11
 US-09-252-991A-8112/c
 Sequence 8112, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: MARC J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
 TITLE OF INVENTION: *AERUGINOSA* FOR DIAGNOSTICS AND THERAPEUTICS
 FILE NUMBER: 107196-136
 FILE REFERENCE: 287
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/074, 788
 PRIOR FILING DATE: 1998-02-18
 US-09-13
 US-09-632-098-5
 Sequence 5, Application US/09632098
 Patent No. 642054

```

; GENERAL INFORMATION:
;   APPLICANT: Sheppard, Paul O.
;   APPLICANT: Bairdur, Nand
;   APPLICANT: Bishop, Paul D.
;   TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
;   FILE REFERENCE: 99-39
;   CURRENT APPLICATION NUMBER: US/09/632,098
;   CURRENT FILING DATE: 2000-08-02
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 5
;   LENGTH: 2406
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Degenerate sequence
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2406)
;   OTHER INFORMATION: n = A,T,C or G
;   US-09-632-098-5

Query Match          3.0†;  Score 32.2;  DB 3;  Length
Best Local Similarity 25.2†;  Pred. No. 11;
Matches 82;  Conservative 47;  Mismatches 197;  Indels 19
Qy          637 CTGCGCAAGGAATGTATCCGATGGCTATTCCATCAAACGCAAT
Db          1016 CNGCNGNACNATGGCNAYGARATHGCNAYWSNTYNGGNTYMSN
Qy          697 GGACCTCTCTCTGATTCGATGGCTTCCGATGATCAGCC
Db          1076 GNTGTYGVTGNGARGCNCNGNARGWSNGNGGNTYGTGNTATGCNC
Qy          757 TTTCGGCGCCGCTTGCCTGCCTCTTACGTTGCCGCTGTCA
Db          1136 ATGCTTACGACCACTCCCTTACAAAGTTCCAAGGAGCGSCTCTGT
Qy          817 ATGGCTTACGACCACTCCCTTACAAAGTTCCAAGGAGCGSCTCTGT
Db          1196 ARGENGNGGNGNTGTYTNNNAATCNCNCNGAYCNCNGENYTNCCN
Qy          877 GTTAGCGTTGCAATTATCAGGGACCTGGTTATGGCTCCAGG
Db          1256 TNGTGGGNAAYGNTTGTGNGARGCNCNGNARGARTGTYGATYGCNN
Qy          937 GTAAACAACGGTAGTTCTGTCATAAT 962
Db          1316 GNGNGAYTNTGTTGTTGNCAY 1341

RESULT 14
US-10-177-308-5
; Sequence 5, Application US/10177308
; Patent No. 6762044
; GENERAL INFORMATION:
;   APPLICANT: Sheppard, Paul O.
;   APPLICANT: Bairdur, Nand
;   APPLICANT: Bishop, Paul D.
;   TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
;   FILE REFERENCE: 99-39
;   CURRENT APPLICATION NUMBER: US/10/177,308
;   CURRENT FILING DATE: 2002-06-21
;   PRIOR APPLICATION NUMBER: US/09/632,098
;   PRIOR FILING DATE: 2000-08-02
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 5
;   LENGTH: 2406
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Degenerate sequence

```

Db 1136 AYCCNTTYCCNGNTTYSNSNGNTGTYWSNMGNMGNCACTNNGNCNTTYTGYNA 1195
Qy 817 ATGGCTAGACCCCTCTTACAAGTGTCCAAGGAGGGCTTGTATCCGTTTCAGAC 876
Db 1196 ARGGNGGGNGCNTGTYTWSNAVGNCCNGAYCCNGNNTNCNGNCCNGNY 1255
Qy 877 GTTAAGGGTTGCGAATTATCAAGAGCGCACTGGTTATGGCTCCGAGCTAAGCTCAGGC 936
Db 1256 TNTGYGNAAGGNTYGTGNGARGCNGNGARGARTGYATGYGENCNGNARGART 1315
Qy 937 GAAACACCGGTAGTTCAATCGTCAAT 962
Db 1316 GYMGNAYTNTGTYTGYTGYNCAY 1341

Search completed: July 9, 2005, 12:58:47
Job time : 207.141 sec_B

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Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	1071	100.0	1071	9	US-09-938-842A-1034	Sequence 1034, Ap
2	1071	100.0	1071	11	US-09-938-842A-1034	Sequence 1034, Ap
C 3	448	41.8	460	9	US-09-924-502	Sequence 502, App
C 4	439	41.0	453	9	US-09-924-446-615	Sequence 615, App
C 5	228.6	21.3	1847	18	US-10-424-599-109777	Sequence 109777, App
C 6	185	18.5	1895	9	US-09-770-696-257	Sequence 8512, App
C 7	183.6	17.1	1990	18	US-10-425-114-8512	Sequence 8512, App
SUMMARIES						
8						
Run on:	July 9, 2005, 12:33:30 ;	Search time	712.441	Seconds	US-10-425-114-14614	Sequence 14614, A
Scoring table:	IDENTITY_NUC	(without alignments)			Sequence 43464, A	
OM nucleic - nucleic search, using sw model		9438.079 Million cell updates/sec			Sequence 3143, Ap	
Title: US-09-938-842A-1034	Perfect score: 1071	Sequence: atggcacaattcgaagct.....cacggttcatcgaaaccatgt	1071		Sequence 63594, A	
Scoring table: Gapext 1.0	Searched: 6330943 seqs, 3139157217 residues	Total number of hits satisfying choosen parameters: 126661886			Sequence 14605, A	
Minimum DB seq length: 0	Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0%	Maximum Match 100%	Listing First 45 summaries		
Database : Published Applications NA:*						
1: /cgn2_6/ptodata/2/pubpna/us07_pubcomb.seq:*					RESULT 1	
2: /cgn2_6/ptodata/2/pubpna/pct_new_pub.seq:*					US-09-938-842A-1034	
3: /cgn2_6/ptodata/2/pubpna/us07_new_pub.seq:*					/ Sequence 1034, Application US/09938842A.	
4: /cgn2_6/ptodata/2/pubpna/us06_pubcomb.seq:*					/ General Information:	
5: /cgn2_6/ptodata/2/pubpna/us07_new_pub.seq:*					/ Patent No. US20030160378A1	
6: /cgn2_6/ptodata/2/pubpna/pctst_pubcomb.seq:*					/ APPLICANT: Harper, Jeff	
7: /cgn2_6/ptodata/2/pubpna/us08_new_pub.seq:*					/ APPLICANT: Krebs, Joel	
8: /cgn2_6/ptodata/2/pubpna/us09_pubcomb.seq:*					/ APPLICANT: Wang, Kun	
9: /cgn2_6/ptodata/2/pubpna/us09_pubcomb.seq:*					/ APPLICANT: Zhu, Tong	
10: /cgn2_6/ptodata/2/pubpna/us09b_pubcomb.seq:*					/ TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING THE SAME, AND METHODS OF USE	
11: /cgn2_6/ptodata/2/pubpna/us09c_pubcomb.seq:*					/ FILE REFERENCE: SCRIP1300-3	
12: /cgn2_6/ptodata/2/pubpna/us09_pub.seq:*					/ CURRENT APPLICATION NUMBER: US/09/938, 842A	
13: /cgn2_6/ptodata/2/pubpna/us10_pubcomb.seq:*					/ PRIORITY FILING DATE: 2001-08-24	
14: /cgn2_6/ptodata/2/pubpna/us10b_pubcomb.seq:*					/ PRIORITY APPLICATION NUMBER: US 60/227, 866	
15: /cgn2_6/ptodata/2/pubpna/us10c_pubcomb.seq:*					/ PRIORITY FILING DATE: 2001-01-16	
16: /cgn2_6/ptodata/2/pubpna/us10_pubcomb.seq:*					/ PRIORITY APPLICATION NUMBER: US 60/300, 111	
17: /cgn2_6/ptodata/2/pubpna/us10e_pubcomb.seq:*					/ PRIORITY FILING DATE: 2001-06-22	
18: /cgn2_6/ptodata/2/pubpna/us10f_pubcomb.seq:*					/ NUMBER OF SEQ ID NOS: 5379	
19: /cgn2_6/ptodata/2/pubpna/us10g_pubcomb.seq:*					/ SEQ ID NO: 1034	
20: /cgn2_6/ptodata/2/pubpna/us10h_pubcomb.seq:*					/ LENGTH: 1071	
21: /cgn2_6/ptodata/2/pubpna/us10i_pubcomb.seq:*					/ TYPE: DNA	
22: /cgn2_6/ptodata/2/pubpna/us10_pub.seq:*					/ ORGANISM: Arabidopsis thaliana	
23: /cgn2_6/ptodata/2/pubpna/us10a_pubcomb.seq:*					US-09-938-842A-1034	
24: /cgn2_6/ptodata/2/pubpna/us11_pub.seq:*						
25: /cgn2_6/ptodata/2/pubpna/us60_new_pub.seq:*						
26: /cgn2_6/ptodata/2/pubpna/us60_pubcomb.seq:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
Scoring table: ALIGNMENTS						

RESULT 2
 US-09-938-842A-1034
 Sequence 1034, Application US/0938842A
 Publication No. US20040009476A9
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeff
 APPLICANT: Kreps, Joe L.
 APPLICANT: Wang, Xun
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 FILE REFERENCE: SCRIP1300-3
 CURRENT APPLICATION NUMBER: US/09/938-842A
 CURRENT FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US 60/227, 866
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/264, 647
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/300, 111
 PRIOR FILING DATE: 2001-06-22
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO 1034
 LENGTH: 1071
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 US-09-938-842A-1034

Query 1 ATGGCGCAATTCAAGAAGCTTGAAGAAGTCAACTCTAAGGCCGTT 60
 Query 1 ATGGCGCAATTCAAGAAGCTTGAAGAAGTCAACTCTAAGGCCGTT 60
 Db 61 GATCTTACCATCTATCAACGGGCTCAAAACCTCGAAACTTCAGAAT 120
 Db 61 GATCTTACCATCTATCAACGGGCTCAAAACCTCGAAACTTCAGAAT 120
 Query 121 CCCACAGTGAAGTCTCGAGCC2AGGCCAGGGTATGCCGCTGTTCAATGTTTA 180
 Query 121 CCCACAGTGAAGTCTCGAGCC2AGGCCAGGGTATGCCGCTGTTCAATGTTTA 180
 Query 181 GCTCCACCGTCTTGAGGAGGCTTCAACTAAAGACCGTCAACG 240
 Query 181 GCTCCACCGTCTTGAGGAGGCTTCAACTAAAGACCGTCAACG 240
 Query 241 AAGGTTAAAGGAAAGGGAGGAGGATACGGATGCGCTGGCTAGGATTTT 300
 Query 241 AAGGTTAAAGGAAAGGGAGGAGGATACGGATGCGCTGGCTAGGATTTT 300
 Query 301 CRATTAACTCGAGAGTAAAGCTTCAAAATCCACGGAAAGATTCGGTGTGGAG 360
 Query 301 CRATTAACTCGAGAGTAAAGCTTCAAAATCCACGGAAAGATTCGGTGTGGAG 360
 Query 361 AACGCTAGCCGGGATTATAGCCGGACGGTACGGAAACGGTCCGCCATGCCATG 420
 Query 361 AACGCTAGCCGGGATTATAGCCGGACGGTACGGAAACGGTCCGCCATGCCATG 420
 Query 421 TCGGTTAACGGAAACCTTAAATCCGACGGGACGGTCACTGGTGA 480
 Query 421 TCGGTTAACGGAAACCTTAAATCCGACGGGACGGTCACTGGTGA 480
 Db 481 AAATCTGATGAAAGAACGTAACGGCCTCTAACAGTGTGTTATAGACATTAACGAC 540
 Query 481 AAATCTGATGAAAGAACGTAACGGCCTCTAACAGTGTGTTATAGACATTAACGAC 540
 Db 481 AAATCTGATGAAAGAACGTAACGGCCTCTAACAGTGTGTTATAGACATTAACGAC 540
 Query 541 GCGGTTCAGTCTCGGTTAGCTCAATTGCACGAGATCCAACTCCG 600
 Query 541 GCGGTTCAGTCTCGGTTAGCTCAATTGCACGAGATCCAACTCCG 600
 Query 601 CAAAGCTCTGGCATCATCACTCTGGCTCAGAACCTCTAACAGTGTGTTATCCGATG 660
 Query 601 CAAAGCTCTGGCATCATCACTCTGGCTCAGAACCTCTAACAGTGTGTTATCCGATG 660
 Db 661 TGGGGTATTCCATCAACGCAATGATGATGAGCTTCTCTGATTCCACAA 720
 Query 661 TGGGGTATTCCATCAACGCAATGATGATGAGCTTCTCTGATTCCACAA 720
 Db 661 TGGGGTATTCCATCAACGCAATGATGATGAGCTTCTCTGATTCCACAA 720
 Query 721 ATCGCTGGTCTCGATCATCGACTCTGGCTCAGAACCTCTAACAA 780
 Query 721 ATCGCTGGTCTCGATCATCGACTCTGGCTCAGAACCTCTAACAA 780
 Query 781 TCGTCCTTACGTCGGCTGTTCAACAGGCTTCACGATGGCTAACAA 840
 Query 781 TCGTCCTTACGTCGGCTGTTCAACAGGCTTCACGATGGCTAACAA 840
 Db 840 TCGTCCTTACGTCGGCTGTTCAACAGGCTTCACGATGGCTAACAA 840
 Query 840 TCGTCCTTACGTCGGCTGTTCAACAGGCTTCACGATGGCTAACAA 840
 Query 841 GTTGTTCAGGAGGGCTTGTATCGGTTCAAGACGTTAGGTTCAATTAAGA 900
 Query 841 GTTGTTCAGGAGGGCTTGTATCGGTTCAAGACGTTAGGTTCAATTAAGA 900
 Db 900 ATTGCAACAAACGAGGCAACGAGGCTAACAGGAGGACTTCTCCCTGAAATTAAAGA 1020
 Query 900 ATTGCAACAAACGAGGCAACGAGGCTAACAGGAGGACTTCTCCCTGAAATTAAAGA 1020
 Db 960 GGGACGTGGGTTATGGTCTCGAGCTCAAGACCGCTAGTCATGTC 960
 Query 960 GGGACGTGGGTTATGGTCTCGAGCTCAAGACCGCTAGTCATGTC 960
 Query 961 ATTGCAACAAACGAGGCAACGAGGCTAACAGGAGGACTTCTCCCTGAAATTAAAGA 1020
 Query 961 ATTGCAACAAACGAGGCAACGAGGCTAACAGGAGGACTTCTCCCTGAAATTAAAGA 1020
 Db 1021 GAGCTTACCAAGCTTCAAGACTGCTTCAAGACTGCTTCAAGACTG 1071
 Query 1021 GAGCTTACCAAGCTTCAAGACTGCTTCAAGACTGCTTCAAGACTG 1071
 Db 1021 GAGCTTACCAAGCTTCAAGACTGCTTCAAGACTGCTTCAAGACTG 1071

LENGTH: 1113
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURE: unsure
 NAME/KEY: (1)..(1113)
 LOCATION: (1)..(1113)
 OTHER INFORMATION: unsure at all n locations
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_139247C.1
 US-10-424-599-43464

Query Match 13.6%; Score 145.2; DB 18; Length 1113;
 Best Local Similarity 64.8%; Pred. No. 2.1e-38;
 Matches 232; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 221 CGACTAAAGACCGTCAAGCAGGGTCAAGGAAAGGAGGAAAGGATACGGATGCCCTGCCA 280
 Db 635 CTCGAGGGATGGCAACGAGGTGGTCAAGGATGGTGGCCAGAAATCAGATGCCGGCA 694
 Qy 281 CGTGTGGGGCTAGGATTTCATTAACTCGAAGCTTACGGTCAAGTGGTCAAAATCCGACGGCAA 340
 Db 695 CTCGCGGGGGGGGGATTCGGCTGAGCGGGAAACTGGCACACAGTGGCGACGGGAA 754
 Qy 341 CGATTCCGGTGGTGTGGTGGAGACGGCTGAGCGCTGAGCGGATTATAAGCCGCAACGGAA 400
 Db 755 CAATTCGGTGGTGTGGTGGAGCGGGCACTTCGGCACTTCGGCAACGGCACCGCA 814
 Qy 401 CGGTTCGGCCATGGCCATGGGGTAACGGGACCTTAAATCCGACGACGAAAGC 460
 Db 815 CAATCCGGGATCGCCATGGGGTAACGGGACCTTAAATCCGACGACGAAAGC 874
 Qy 461 CTGATTCGTGATGGTGAATACTGTGAGAAGAAACTTAACGCTCTAACAGTC 520
 Db 875 CAAGACCCGGAGGAGAGTGCACACTCCGAAAAGGAAAGGAGGAGCTCAACAGCG 934
 Qy 521 AGTATATAAGATAAAAGG--ACGGCGTTTAAGCTCTCGGTTAGCTCAATTGC 575
 Db 935 AATTATCGACGTGAAAGAAAACCGGTTCTGTCTCTGGCTGCCAACATGC 992

FEATURE:
 OTHER INFORMATION: Glycine max

RESULT 10
 US-10-739-930-3143
 ; Sequence 3143, Application US/10739930
 ; Publication No. US20040216190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
 ; FILE REFERENCE: 38-21(53377)B
 ; CURRENT APPLICATION NUMBER: US/10/739,930
 ; CURRENT FILING DATE: 2003-12-18
 ; NUMBER OF SEQ ID NOS: 11088
 ; SEQ ID NO 3143
 ; LENGTH: 1616
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER131780_1
 US-10-739-930-3143

Query Match 13.5%; Score 144.8; DB 20; Length 1616;
 Best Local Similarity 63.5%; Pred. No. 3.6e-38;
 Matches 240; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

Qy 202 CCACCATGAGAGGCTTCACTAAAGCGGTCAACGAGGTGAAGGAGGGAGA 261
 Db 399 CCTCCACGAAGAACCCGCAACCAAAGTGGAAAGGGGGGAAAGTGGAGGCC 458
 Qy 262 AGGATAGGATCTGGCACCTGGTGGCTAGGATTTGAACTCGAGTTAGGT 321
 Db 459 AGGATCCGATTAACCGGCCACCTGGCCTGGCTGGCGGGATTTCCAGGTGAGGTGGCG 518
 Qy 322 CACAAATCCGACGGGAAACGATTGATTGATTGCGGTTGTTGAGGAGCGCTGATTATA 381

Query Match 13.6%; Score 145.2; DB 18; Length 1113;
 Best Local Similarity 64.8%; Pred. No. 2.1e-38;
 Matches 232; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 502 AAACGAACTCTAACAGTGAAGTGTAAAGCTTACAGTGGCTTTTCAGCTTCC 555
 Db 639 ATCCCAACCACCTCATGAGACGCTTCGGGACATAAACATAAACAGGCGG 698

Query Match 13.6%; Score 145.2; DB 18; Length 1113;
 Best Local Similarity 64.8%; Pred. No. 2.1e-38;
 Matches 232; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 502 AAACGAACTCTAACAGTGAAGTGTAAAGCTTACAGTGGCTTTTCAGCTTCC 555
 Db 699 AAACGCCCTCAAAAGCAGGTTGTTGGACATAAAACATAAACAGGCGG 728

Query Match 13.6%; Score 145.2; DB 18; Length 1113;
 Best Local Similarity 64.8%; Pred. No. 2.1e-38;
 Matches 232; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 502 AAACGAACTCTAACAGTGAAGTGTAAAGCTTACAGTGGCTTTTCAGCTTCC 555
 Db 755 TCCGGTTGCTGCCGGTT 776

RESULT 11
 US-10-424-599-63594
 ; Sequence 63594, Application US/10424599
 ; Publication No. US2004031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 28564
 ; SEQ ID NO 63594
 ; LENGTH: 1594
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28439C.1
 US-10-424-599-63594

Query Match 12.9%; Score 138; DB 18; Length 1594;
 Best Local Similarity 64.6%; Pred. No. 7.9e-36;
 Matches 248; Conservative 0; Mismatches 115; Indels 21; Gaps 2;

Qy 211 AAGAGACGTTGACTAAAGCGGTCAACGAAGTTGAGGAAGGAAAGTACGG 270
 Db 369 AAGGCGCTCCCTCACGAAAGGACCGCCACACAAAGTGGAGGGCGGGCGAGATCCGA 428
 Qy 271 ATGGCTGCCAGTGTGCGGTAGATTTCATAATCTGAGGTAGTGTACAAATCC 330
 Db 429 ATACCGGCCACCTGGCCGGGCAATTCGCACTGGCCAGCTTCAGTGC 488
 Qy 331 GACGCGAAAGCAGATCGGTGTTGGGAACCTGAGCCGGCATPATAGCGCGCAGC 390
 Db 489 GACGCGGAGACCCGCTGGCTGGCATGGCCATGGGCGGCTCATCTGAGGCACCC 548

Query Match 13.5%; Score 144.8; DB 20; Length 1616;
 Best Local Similarity 63.5%; Pred. No. 3.6e-38;
 Matches 240; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

Qy 391 GGTAAGGAAAGCTTCACTAACAGTGGTAACTGCGTAACTTAAATCCGACCG 450
 Db 549 GGCAACGGCAGCTGGCATGGCTCGGCTCGGCTGGGCGGCTCAAATCCAAAC 608
 Qy 451 AC-----GACGAACCTGATTCGTTATGGCTGAAATCTGATGAGAAAGAACGT 501
 Db 609 ACCTGATCCAACTCTAACAGGAGACCCGCGCTCCTCCACAAAGAGCGG 668

Query Match 13.5%; Score 144.8; DB 20; Length 1616;
 Best Local Similarity 63.5%; Pred. No. 3.6e-38;
 Matches 240; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

Qy 502 AAACGAACTCTAACAGTGAAGTGTAAAGCTTACAGTGGCTTTTCAGCTTCC 549
 Db 669 AAACGCCCTCAAAAGCAGGTTGTTGGACATAAAACATAAACAGGCGG 728

Query Match 13.5%; Score 144.8; DB 20; Length 1616;
 Best Local Similarity 63.5%; Pred. No. 3.6e-38;
 Matches 240; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

Qy 502 AAACGAACTCTAACAGTGAAGTGTAAAGCTTACAGTGGCTTTTCAGCTTCC 549
 Db 550 GCTTCCTCCGGTTAGCTCAAAT 573

Db 729 CAGTCGTCGGCTGGCCCCGGTT 752

RESULT 12

US-10-425-114-14605

Sequence 14605, Application US/10425114

Publication No. US20040034886A1

GENERAL INFORMATION

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5331)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 73128

LENGTH: 1519

TYPE: DNA

ORGANISM: *Arabidopsis thaliana*

FEATURE: PEPTIDE

OTHER INFORMATION: Clone ID: LIB23-047-E8_FLI

US-10-425-114-14605

Query Match 12.0%; Score 129; DB 18; Length 1519;

Best Local Similarity 71.0%; Pred. No. 9.7e-33; Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Db 68 GGGAGCTAAAAGCCAAGTGTGAAACCGGACATGGTGA 127

Qy 189 GTCCTCGACAGGACCACTTGGAGAGCTTGACTTAAGACCGTCAACAGGAAGGTTGA 248

Db 128 CGGAAGGGGGAGGATAAGGTTACGGATGCTGGCTAGATTTCAATTAAAC 308

Qy 309 TCGAGAGTTAGCTACAATTCGAACTGGCAAGAACGATTGGTGGAACTCTGA 368

Db 540 GCGGAGGCTAGGTCTAAATCGGAGGTGACAATAGATGGCTCTTCGAACTGTGA 599

Qy 369 GCGGGGATTATAGGGCCACGGTTACGGGAACGGTCCCCATGCCCCATGCGCTTAA 428

Db 600 ACCATCTGTAATGGCCACCGGACATCCGGACATTCGAACTTCACTTCTTTAA 659

Qy 429 C 429

Db 660 C 660

RESULT 14

US-10-225-068-165

Sequence 165, Application US/10225068

Publication No. US20030217383A1

GENERAL INFORMATION

APPLICANT: Mendel Biotechnology, Inc.

APPLICANT: Reuber, T. Lynn

APPLICANT: Riechmann, Jose Luis

APPLICANT: Heard, Jacqueline E.

APPLICANT: Jiang, Cai-Zhong

APPLICANT: Adam, Luc J.

APPLICANT: Dubell, Arnold T.

APPLICANT: Ratcliffe, Oliver

APPLICANT: Pineda, Omaira

APPLICANT: Yu, Guo-Liang

APPLICANT: Brown, Pierre E.

TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

FILE REFERENCE: 514442002040

CURRENT APPLICATION NUMBER: US/10/225,068

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: 60/310,847

PRIOR FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: 60/336,049

PRIOR FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/338,692

PRIOR FILING DATE: 2001-12-11

PRIOR APPLICATION NUMBER: 10/171,468

PRIOR FILING DATE: 2002-06-14

RESULT 13

US-09-934-455-169

Sequence 169, Application US/09934455

Publication No. US20030121070A1

GENERAL INFORMATION

APPLICANT: Adam, Luc

APPLICANT: Creeiman, Robert

APPLICANT: Dubell, Arnold

APPLICANT: Heard, Jacqueline

APPLICANT: Jiang, Cai-Zhong

APPLICANT: Keddie, James

APPLICANT: Pilgrim, Marsha

APPLICANT: Ratcliffe, Oliver

APPLICANT: Reuber, Lynn

APPLICANT: Riechmann, Jose Luis

APPLICANT: Yu, Guo-Liang

APPLICANT: Pineda, Omaira

TITLE OF INVENTION: Genes for Modifying Plant Traits IV

FILE REFERENCE: MBI-0025

CURRENT APPLICATION NUMBER: US/09/934,455

NUMBER OF SEQ ID NOS: 246
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 165
 LENGTH: 1728
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (106) ... (1575)
 US-10-225-068-165

Query Match 12.0%; Score 129; DB 17; Length 1728;
 Best Local Similarity 71.0%; Pred. No. 1e-32;
 Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 169 GCTTCGAGGACCAATTGAGAGGCTTGACTAAAGCCGTCACCAAGTTGA 248
 Db 420 GGGAGCTAAAAGCCACCGTTGAAACGCCGACACGAAAGCTGA 479

Qy 249 AGGAAGACGGAGGGAGGGATAACGGATGCCACGTGCGGTAGGATTTCAATTAC 308
 Db 480 CGGAAGAGGGAGGAATAAGATGGCTATGTCAGTAGGTTTCACTAAC 539

Qy 309 TCGAGACTTAGCTCAAAATCCGACGCCAACGATTCGGTGTGTTGGAAACGCTGA 368
 Db 540 GCGAGAGCTTAGGTCTAAATCCGACGGTACAATGGTGGCTTCTCAACAAAGCTGA 599

Qy 369 GCGGGCGTTATAGCCGCACCGTAAAGGTTCCGCACTCCCAGTCGCTTAA 428
 Db 600 ACCATCTCTTAATGCCGCCACCGGAACCGGAACAATTCCGGGAATTTCACCTCTTTAA 659

Qy 429 C 429
 Db 660 C 660

RESULT 15
 US-10-574-780A-219
 Sequence 219, Application US/10374780A
 GENERAL INFORMATION
 Publication No. US20040019927A1

APPLICANT: Sherman, Bradley K
 APPLICANT: Riechmann, Jose Luis
 APPLICANT: Jiang, Cai-Zhong
 APPLICANT: Heard, Jacqueline E
 APPLICANT: Haake, Volker
 APPLICANT: Creelman, Robert A
 APPLICANT: Ratcliffe, Oliver
 APPLICANT: Adam, Luis J
 APPLICANT: Reuber, T. Lynne
 APPLICANT: Keddie, James
 APPLICANT: Brown, Pierre E
 APPLICANT: Pilgrim, Marsha L
 APPLICANT: Dubell, III, Arnold T
 APPLICANT: Pineda, Omaira
 APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
 FILE REFERENCE: MBI-0047 CIP
 CURRENT APPLICATION NUMBER: US/10/374,780A
 CURRENT FILING DATE: 2003-02-25
 PRIOR APPLICATION NUMBER: 09/837,944
 PRIOR FILING DATE: 2001-04-18
 PRIOR APPLICATION NUMBER: 60/310,847
 PRIOR FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/934,455
 PRIOR FILING DATE: 2001-08-22
 PRIOR APPLICATION NUMBER: 60/336,049
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/338,692
 PRIOR FILING DATE: 2001-12-11
 PRIOR APPLICATION NUMBER: 10/171,468
 PRIOR FILING DATE: 2002-06-14
 PRIOR APPLICATION NUMBER: 10/225,066

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	20	1.9	78810	4	US-09-949-016-16198	Sequence 16198, A	Sequence 16198, A	
2	19	1.8	2555	4	US-09-419-039A-6112	Sequence 6112, AP	Sequence 6112, AP	
3	19	1.8	34094	4	US-09-292-034-1	Sequence 1, Appli	Sequence 1, Appli	
c	19	1.8	168394	4	US-09-945-016-13002	Sequence 1, Appli	Sequence 1, Appli	
5	18	1.7	372	4	US-09-905-540-5948	Sequence 5948, AP	Sequence 5948, AP	
6	18	1.7	1527	4	US-09-489-039A-716	Sequence 716, APP	Sequence 716, APP	
7	18	1.7	1720	4	US-09-905-540-198	Sequence 198, APP	Sequence 198, APP	
c	18	1.7	4261	4	US-09-905-540-198	Sequence 3, Appli	Sequence 3, Appli	
c	9	18	1.7	35685	4	US-09-949-016-16873	Sequence 16873, A	Sequence 16873, A
c	10	18	1.7	94879	4	US-09-949-016-12101	Sequence 12101, A	Sequence 12101, A
c	11	18	1.7	94884	4	US-09-949-016-13333	Sequence 13333, A	Sequence 13333, A
c	12	18	1.7	162440	3	US-09-345-882-1	Sequence 1, Appli	Sequence 1, Appli
c	13	18	1.7	784019	4	US-09-949-016-14033	Sequence 14033, A	Sequence 14033, A
c	14	18	1.7	828152	4	US-09-949-016-12777	Sequence 12777, A	Sequence 12777, A
c	15	18	1.7	1664976	4	US-09-916-421B-1	Sequence 1, Appli	Sequence 1, Appli
c	16	18	1.7	1664976	4	US-09-602-570-1	Sequence 24082, A	Sequence 24082, A
c	17	1.6	318	4	US-09-513-99C-24082	Sequence 1834, AP	Sequence 1834, AP	
c	18	1.7	1.6	338	4	US-09-640-211A-1834	Sequence 12761, AP	Sequence 12761, AP
c	19	1.6	396	4	US-09-248-796A-12761	Sequence 186, APP	Sequence 186, APP	
c	20	17	1.6	447	4	US-09-282-352-186	Sequence 454, APP	Sequence 454, APP
c	21	17	1.6	494	4	US-09-220-767-454	Sequence 15736, A	Sequence 15736, A
c	22	17	1.6	494	4	US-09-210-767-454	Sequence 2, Appli	Sequence 2, Appli
c	23	17	1.6	516	4	US-08-916-421B-1	Sequence 178644, Sequence 178645, Sequence 178646, Sequence 184362,	Sequence 178644, Sequence 178645, Sequence 178646, Sequence 184362,
c	24	17	1.6	601	4	US-09-949-016-178844	Sequence 1, Appli	Sequence 1, Appli
c	25	17	1.6	601	4	US-09-949-016-178845	Sequence 1, Appli	Sequence 1, Appli
c	26	17	1.6	601	4	US-09-949-016-178846	Sequence 1, Appli	Sequence 1, Appli
c	27	17	1.6	601	4	US-09-949-016-184362	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-16198
; Sequence 16198, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09-949-016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16198
; LENGTH: 78810
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)_(78810)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-16198

Query Match 1.9%; Score 20; DB 4; Length 78810;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1029 CCAGTTCATGACCAACAA 1048
Db 17829 CCAGTTCATGACCAACAA 17848

RESULT 2
US-09-489-039A-6112
; Sequence 6112, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709 2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747

OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13002

Query Match 1.8%; Score 19; DB 4; Length 168394;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 545 TTTCAGCTTCCCGCTTT 563
Db 77366 TTTCAGCTTCCCGCTTT 77348

RESULT 5
US-09-902-540-5948
; Sequence 5948, Application US/09902548
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5948
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-5948

Query Match 1.7%; Score 18; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 GCGGTGATGCCGTGCTT 167
Db 234 GCGGTGATGCCGTGCTT 251

RESULT 6
US-09-489-039A-716
; Sequence 716, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 1442
; SEQ ID NO 716
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-716

Query Match 1.7%; Score 18; DB 4; Length 1527;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 AGGCCAGCCGGTGTGTC 160
Db 965 AGGCAGCCGGTGTGTC 982

RESULT 7

OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12002/c

Sequence 13002, Application US/09949016

GENERAL INFORMATION:
; Patent No. 6812339
; APPLICANT: VENTER, J. Craig et. al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13002
; LENGTH: 168394
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(168394)

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US-09-902-540-198
; Sequence 138, Application US/09902540
; Patent No. 683347
GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10 (15849) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 198
LENGTH: 1720
TYPE: DNA
ORGANISM: Myxococcus xanthus
us-09-902-540-198

Query Match 1.7%; Score 18; DB 4; Length 1720;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 10
US-09-949-016-12101/c
; Sequence 12101, Application US/09949016
Db 2314 GCGGGTGTGCCCCCTCGTT 251

RESULT 8
US-09-976-594-3/c
; Sequence 3, Application US/09976594
; Patent No. 6673549
GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELLS TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 4261
TYPE: DNA
FEATURE: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 18633316CB1
us-09-976-594-3

Query Match 1.7%; Score 18; DB 4; Length 4261;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 9
US-09-949-016-16873/c
; Sequence 16873, Application US/09949016
; Patent No. 6812339
GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16873
LENGTH: 35688
TYPE: DNA
ORGANISM: Human
US-09-949-016-16873

Query Match 1.7%; Score 18; DB 4; Length 35688;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 473 TGGTGAATCTGATCA 490
Db 30454 TGGTGAATCTGATCA 30437

RESULT 11
US-09-949-016-12101/c
; Sequence 12101, Application US/09949016
; Patent No. 6812339
GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12101
LENGTH: 94879
TYPE: DNA
ORGANISM: Human
FEATURE: misc feature
NAME/KEY: (1)_(94879)
LOCATION: (1)_(94879)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12101

Query Match 1.7%; Score 18; DB 4; Length 94879;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 510 TTCTAACAGTGATAT 527
Db 76650 TTCTAACAGTGATAT 76633

RESULT 12
US-09-949-016-13393/c
; Sequence 13393, Application US/09949016
; Patent No. 6812339
GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

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PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 13333
LENGTH: 94884
TYPE: DNA
ORGANISM: Human
FEATURE: misc_feature
NAME/KEY: (1)_-(94884)
LOCATION: n = A,T,C or G
US-09-949-016-13393

Query Match 1.7%; Score 18; DB 4; Length 94884;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 510 TCTTAAGCTGAGTATAT 527
Db 76650 TCTTAAGCTGAGTATAT 76633

RESULT 12
US-09-345-882-1
Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEAR ACID.
FILE REFERENCE: GENSSET 031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIORITY APPLICATION NUMBER: US 60/091,315
PRIORITY FILING DATE: 1998-06-10
PRIORITY APPLICATION NUMBER: US 60/111,909
PRIORITY FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent-PM

SEQ ID NO 1
LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 98050 .88096
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 72771 .72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 16031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 143374
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134346
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 16031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771 .72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771 .72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050 .88096
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele

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LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 91690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 98075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130

```

OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108127..108177
 OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108127..108177
 OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
 FEATURE:
 Query Match 1 ; Score 18 ; DB 3 ; Length 162450 ;
 Best Local Similarity 100.0% ; Pred. No. 46 ;
 Matches 18 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
 Qy 695 TCGGAGCTTCCTCTCTGCA 712
 Db 35413 TCGGAGCTTCCTCTGCA 35430

RESULT 13
 US-09-949-016-14033/C
 Sequence 14033, Application US/0949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIORITY NUMBER: CL001307
 PRIORITY FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-09-08
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 14033
 LENGTH: 784019
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(784019)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-14033

Query Match 1 ; Score 18 ; DB 4 ; Length 784019 ;
 Best Local Similarity 100.0% ; Pred. No. 44 ;
 Matches 18 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
 Qy 985 CTGAGAGACTCTCCCTA 1002
 Db 136173 CTGAGAGACTCTCCCTA 136156

RESULT 14
 US-09-949-016-12777/C
 Sequence 12777, Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-09-08
 PRIOR FILING DATE: 2000-09-08

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; PRIORITY NUMBER: 60/231,498
; PRIORITY DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PassSEQ for Windows Version 4.0
; SEQ ID NO: 12777
; LENGTH: 828152
; TYPE: DNA
; ORGANISM: Human
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1).828152
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-12777

Query Match 1.7% Score 18; DB 4; Length 828152;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 985 CTCAGAGACTTCTCCCTA 1002
Db 132306 CTCAGAGACTTCTCCCTA 132289

RESULT 15
US-08-916-421B-1/C
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Built et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: P275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; NAME/KEY: misc_feature
; LOCATION: (288252).28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (288257).28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84773).84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98170).98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (848159).84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98239).98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98256).98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98343).98343)

; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (103998).103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (148948).148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (163395).163395)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191989).191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (191995).191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (231980).231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234187).234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234220).234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (234814).234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309398).309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (309418).309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
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US-08-916-421B-1

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GenCore version 5.1.6
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ON nucleic - nucleic search, using SW model

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(without alignments)
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Perfect score: 1071
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 6330943 seqs, 3139157217 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12661886

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1071	100.0	1071	9 US-09-938-842A-1034	Sequence 1034, Ap
2	100.0	1071	11 US-09-938-842A-1034	Sequence 1034, Ap	
3	28.9	27.0	460	9 US-09-934-038A-502	Sequence 502, Ap
4	28.6	26.7	453	9 US-09-770-444-615	Sequence 615, APP
5	18.5	17.3	185	9 US-09-770-696-257	Sequence 257, APP
6	25	2.3	704	17 US-10-225-066A-1049	Sequence 1049, Ap
7	25	2.3	704	17 US-10-374-780A-2689	Sequence 2689, Ap

ALIGNMENTS

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; Patent No. US20160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/938, 842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1034
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1034
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 ; Sequence 1034, Application US/09/38842A
 ; Publication No. US2004009476A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joe L
 ; APPLICANT: Wang, Kun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: Sкрип1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
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; APPLICANT: An, Yong-Qiang						
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; APPLICANT: Price, Jennifer L.						
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; APPLICANT: Hurban, Patrick						
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US-09-770-444-615						
Query Match Score 286; DB 9; Length 453;						
Best Local Similarity 100.0%; Pred. No. 6.7e-147; Mismatches 0; Indels 0; Gaps 0;						
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
; NAME/KEY: misc_feature						
; LOCATION: (1)...(453)						
; OTHER INFORMATION: n = A,T,C or G						
US-09-770-444-615						
Query Match Score 286; DB 9; Length 453;						
Best Local Similarity 100.0%; Pred. No. 6.7e-147; Mismatches 0; Indels 0; Gaps 0;						
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
; NAME/KEY: misc_feature						
; LOCATION: (1)...(453)						
; OTHER INFORMATION: n = A,T,C or G						
US-09-770-444-615						
Query Match Score 286; DB 9; Length 453;						
Best Local Similarity 100.0%; Pred. No. 6.7e-147; Mismatches 0; Indels 0; Gaps 0;						
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
; NAME/KEY: misc_feature						
; LOCATION: (1)...(453)						
; OTHER INFORMATION: n = A,T,C or G						
US-09-770-444-615						
Query Match Score 286; DB 9; Length 453;						
Best Local Similarity 100.0%; Pred. No. 6.7e-147; Mismatches 0; Indels 0; Gaps 0;						
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
; NAME/KEY: misc_feature						
; LOCATION: (1)...(453)						
; OTHER INFORMATION: n = A,T,C or G						

Db 226 T₂ACAAGTGT₃CAAGGAGCC₄TGGT₅TAGGT₆CGGTCAGCT₇CAACGGTAA₈ACCGGTAGT₉TCAGGTT₁₀AGC₁₁GTT₁₂CGA₁₃TTA 167

Db 166 T₂CAAGGGACGTGGT₃CAAGGAGCC₄TGGT₅TAGGT₆CGGTCAGCT₇CAACGGTAA₈ACCGGTAGT₉TCAGGTT₁₀AGC₁₁GTT₁₂CGA₁₃TTA 107

Db 106 T₂CAAGGGACGTGGT₃CAAGGAGCC₄TGGT₅TAGGT₆CGGTCAGCT₇CAACGGTAA₈ACCGGTAGT₉TCAGGTT₁₀AGC₁₁GTT₁₂CGA₁₃TTA 1014

Db 1015 AAACAAAGAGCTTCAACAGAGTTCAATGAGCAACACGACCGTCAAT 1060

Db 46 AAACAAAGAGCTTCAACAGAGTTCAATGAGCAACACGACCGTCAAT 1

RESULT 5
US-09-770-696-257
; Sequence 257, Application US/09770696

; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick

; TITLE OF INVENTION: Expressed Sequences of *Arabidopsis*
; TITLE OF INVENTION: *thaliana*

FILE REFERENCE: 20311US (PARA-0202RV)
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 911
SOFTWARE: Past-SEQ for Windows Version 4.0
SEQ ID NO 257
LENGTH: 185

; TYPE: DNA
; ORGANISM: *Arabidopsis thaliana*

US-09-770-696-257

Query Match 17.3%; Score 185; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.4e-91; Mismatches 0; Indels 0; Gaps 0;

Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 GCAAGAGTCAA₂ACTCTAA₃GAGCCG₄TGATCTAACCATCAT₅CAACGGCGTCAGAA₆ACGT₇CG 94

Db 1 GCAAGAGTCAA₂ACTCTAA₃GAGCCG₄TGATCTAACCATCAT₅CAACGGCGTCAGAA₆ACGT₇CG 60

Qy 95 AAACCTCAAGACCTT₂CCAA₃TAATCCACAGT₄GATCT₅CAACGGCGTCAGAA₆ACGT₇CG 154

Db 61 AAACCTCAAGACCTT₂CCAA₃TAATCCACAGT₄GATCT₅CAACGGCGTCAGAA₆ACGT₇CG 120

Qy 155 TGTGCGCTCGTTTCAATGCTT₂CCACGGCGTCAGAA₃ACGT₄GATCT₅CAACGGCGTCAGAA₆ACGT₇CG 214

Db 121 TGTGCGCTCGTTTCAATGCTT₂CCACGGCGTCAGAA₃ACGT₄GATCT₅CAACGGCGTCAGAA₆ACGT₇CG 180

Qy 215 GAGCT 219

RESULT 6
US-10-225-066A-1049
; Sequence 1049, Application US/10225066A

; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREAMAN, Robert A
; APPLICANT: PINEDA, Omaira A
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants

FILE REFERENCE: MB100316-2 US
CURRENT APPLICATION NUMBER: US/10/225, 066A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837, 444
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310, 847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336, 049
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338, 692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171, 468
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1049
LENGTH: 704

; TYPE: DNA
; ORGANISM: *Arabidopsis thaliana*

US-10-225-066A-1049

Query Match 2.3%; Score 25; DB 17; Length 704;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 GACTAAGACCGTCACGAGGTT 246

Db 189 GACTAAGACCGTCACGAGGTT 213

RESULT 7
US-10-374-780A-2689
; Sequence 2689, Application US/10374780A

; Publication No. US2004019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Hake, Volker
; APPLICANT: CREAMAN, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: ADAM, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: BROWN, Pierre E
; APPLICANT: Dubell, III, Arnold T
; APPLICANT: PINEDA, Omaira A
; APPLICANT: YU, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

FILE REFERENCE: MBI-0047 CIP
 CURRENT APPLICATION NUMBER: US/10/374,780A
 CURRENT FILING DATE: 2003-05-25
 PRIORITY APPLICATION NUMBER: 09/837,944
 PRIORITY FILING DATE: 2001-04-18
 PRIORITY APPLICATION NUMBER: 60/310,847
 PRIORITY FILING DATE: 2001-08-09
 PRIORITY APPLICATION NUMBER: 09/934,455
 PRIORITY FILING DATE: 2001-08-22
 PRIORITY APPLICATION NUMBER: 60/336,049
 PRIORITY FILING DATE: 2001-11-19
 PRIORITY APPLICATION NUMBER: 60/338,692
 PRIORITY FILING DATE: 2001-12-11
 PRIORITY APPLICATION NUMBER: 10/171,468
 PRIORITY FILING DATE: 2002-06-14
 PRIORITY APPLICATION NUMBER: 10/225,066
 PRIORITY FILING DATE: 2002-08-09
 PRIORITY APPLICATION NUMBER: 10/225,067
 PRIORITY FILING DATE: 2002-08-09
 PRIORITY APPLICATION NUMBER: 10/225,068
 PRIORITY FILING DATE: 2002-08-09
 NUMBER OF SEQ ID NOS: 2906
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 2689
 LENGTH: 704
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 FEATURE: OTHER INFORMATION: G1663
 US-10-374-780A-2689

Query Match 2.3%; Score 25; DB 17; Length 704;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 GACTAAGACCGTCACAGGAAGTT 246
 Db 189 GACTAAGACCGTCACAGGAAGTT 213

RESULT 8
 US-09-732-627A-4287
 Sequence 4287, Application US/09732627A
 Publication No. US20040123338A1
 GENERAL INFORMATION:
 APPLICANT: Fincher, Karen L.
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with Plants
 FILE REFERENCE: 38-21(51770)B
 CURRENT APPLICATION NUMBER: US/09/732,627A
 CURRENT FILING DATE: 2000-12-08
 NUMBER OF SEQ ID NOS: 4930
 SEQ ID NO: 4287
 LENGTH: 390
 TYPE: DNA
 ORGANISM: *Gossypium hirsutum*
 FEATURE: OTHER INFORMATION: Clone ID: LIB3493-028-P1-M1-F9
 US-09-732-627A-4287

Query Match 2.1%; Score 23; DB 11; Length 390;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 ACTAAAGACCGTCACAGGAAGTT 245
 Db 43 ACTAAAGACCGTCACAGGAAGTT 65

RESULT 9
 US-10-021-323-15482
 Sequence 15482, Application US/10021323
 Publication No. US20040123340A1

GENERAL INFORMATION:
 APPLICANT: Deikman, Jill
 APPLICANT: Feng, Paul C.C.
 APPLICANT: Fincher, Karen L.
 APPLICANT: Ziegler, Todd B.
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants
 FILE NUMBER: 38-21(52274)B
 CURRENT APPLICATION NUMBER: US/10/021,323
 CURRENT FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: US 60/255, 619
 PRIOR FILING DATE: 2000-12-14
 NUMBER OF SEQ ID NOS: 17880
 SEQ ID NO 15482
 LENGTH: 587
 TYPE: DNA
 ORGANISM: *Gossypium hirsutum*
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3829-026-Q6-K6-G6
 US-10-021-323-15482

Query Match 2.1%; Score 23; DB 19; Length 587;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 ACTAAAGACCGTCACAGGAAGTT 245
 Db 257 ACTAAAGACCGTCACAGGAAGTT 279

RESULT 10
 US-10-767-795-3984
 Sequence 3984, Application US/10767795
 Publication No. US20040181830A1
 GENERAL INFORMATION:
 APPLICANT: Kovalic, David K.
 APPLICANT: Cao, Yongwei
 APPLICANT: Zhou, Yinhua
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
 FILE REFERENCE: 38-21(53534)B
 CURRENT APPLICATION NUMBER: US/10/757,795
 CURRENT FILING DATE: 2004-01-30
 NUMBER OF SEQ ID NOS: 117536
 SEQ ID NO 3984
 LENGTH: 938
 TYPE: DNA
 ORGANISM: *Gossypium hirsutum*
 FEATURE:
 OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C3741_1
 US-10-767-795-3984

Query Match 2.1%; Score 23; DB 19; Length 938;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 ACTAAAGACCGTCACAGGAAGTT 245
 Db 258 ACTAAAGACCGTCACAGGAAGTT 280

RESULT 11
 US-10-295-403-147
 Sequence 147, Application US/10295403
 Publication No. US2003010181A1
 GENERAL INFORMATION:
 APPLICANT: Heard, Jacqueline
 APPLICANT: Riechmann, Jose Luis
 APPLICANT: Adam, Luc
 APPLICANT: Brown, Pierre
 APPLICANT: Pineda, Onaira
 APPLICANT: Reuber, Lynne
 APPLICANT: Jiang, Cai-Zhong

APPLICANT: Keddie, James
 APPLICANT: Zhang, James
 APPLICANT: Benito, Maria-Itres
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Fromm, Mike
 TITLE OF INVENTION: PLANT GENE SEQUENCES I
 FILE REFERENCE: MB1-0003
 CURRENT APPLICATION NUMBER: US/10/295,403
 CURRENT FILING DATE: 2002-11-15
 PRIOR APPLICATION NUMBER: US/09/394,519
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: 60/101,349
 PRIOR FILING DATE: 1998-09-12
 PRIOR APPLICATION NUMBER: 60/103,312
 PRIOR FILING DATE: 1998-10-06
 PRIOR APPLICATION NUMBER: 60/108,734
 PRIOR FILING DATE: 1998-11-17
 PRIOR APPLICATION NUMBER: 60/113,409
 PRIOR FILING DATE: 1998-12-22
 NUMBER OF SEQ ID NOS: 170
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 147
 LENGTH: 1604
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (143)..(1345)
 OTHER INFORMATION: G802
 US-10-295-403-147

Query Match Score 2.1%; Best Local Similarity 100.0%; Pred. No. 0.17; Length 1604;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 TCGACTAAAGACCGTCAACGAA 242
 Db 317 TCGACTAAAGACCGTCAACGAA 339

RESULT 13
 US-10-363-345A-33693/c
 Sequence 33693, Application US/10363345A
 ; Publication No. US2004234960A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek
 ; INVENTION: Method for determining the degree of methylation of defined
 ; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3'
 ; FILE REFERENCE: E01/1227
 ; CURRENT APPLICATION NUMBER: US/10/363,345A
 ; CURRENT FILING DATE: 2003-03-03
 ; NUMBER OF SEQ ID NOS: 40712
 ; SEQ ID NO: 33693
 ; LENGTH: 755
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (*Homo sapiens*)
 ; SEQ ID NO: 33693
 ; LENGTH: 345A-33693

Query Match Score 2.0%; Best Local Similarity 100.0%; Pred. No. 2.1%; Length 755;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 438 AAAATCCCGACGAGCAGAA 458
 Db 88 AAAATCCCGACGAGCAGAA 68

RESULT 14
 US-10-363-345A-33694
 Sequence 33694, Application US/10363345A
 ; Publication No. US2004234960A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock
 APPLICANT: Kurt Berlin
 TITLE OF INVENTION: Method for determining the degree of methylation of defined cytosines in genomic DNA in the sequence context of 5'-CpG-3' FILE REFERENCE: E01/1227
 CURRENT APPLICATION NUMBER: US/10/363,345A
 CURRENT FILING DATE: 2003-03-03
 NUMBER OF SEQ ID NOS: 40712
 SEQ ID NO 33694
 LENGTH: 755
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
 OTHER INFORMATION: Cpg-island No: 33694
 US-10-363-345A-33694

Query Match 2.0%; Score 21; DB 20; Length 755;
 Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 438 AAAAATCCGACGAGCGAA 458
 Db 668 AAAAATCCGACGAGCGAA 688

RESULT 15
 US-10-363-483A-33693/C
 Sequence 33693, Application US/10363483A
 Publication No. US20050064401A1
 GENERAL INFORMATION:
 APPLICANT: Alexander Olek
 APPLICANT: Christian Piepenbrock
 APPLICANT: Kurt Berlin
 TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain illnesses
 FILE REFERENCE: E2011
 CURRENT APPLICATION NUMBER: US/10/363,483A
 CURRENT FILING DATE: 2003-03-03
 NUMBER OF SEQ ID NOS: 40712
 SEQ ID NO 33693
 LENGTH: 755
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
 OTHER INFORMATION: Cpg-island No: 33693
 US-10-363-483A-33693

Query Match 2.0%; Score 21; DB 21; Length 755;
 Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 438 AAAAATCCGACGAGCGAA 458
 Db 88 AAAAATCCGACGAGCGAA 68

Search completed: July 9, 2005, 21:43:32
 Job time : 716.441 secs

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